

O'Bryen, Barbara

From: Seharaseyon, Jegatheesan
Sent: Friday, February 28, 2003 5:46 PM
To: O'Bryen, Barbara
Subject: Re:Comparison

Importance: High

Hi Barb,

If you have not done the comparson please do so for the following SEQ ID NO: 1 of 08/828,922 (Patent NO;5,834,240) vs. SEQ ID NO; 2 of 09/856,836. Sorry I gave the wrong seq ID earlier. Thanks a lot.

Seyon.

J.Seharaseyon

Art Unit 1647

CM1 10D16

10B19 MB

Phone:(703)-305-1112

Fax: (703)-746-5177

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

BoSB
3-3-03

> 0 <
01 10 Intelligenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-08-828-922-1.res made by bobryen on Mon 3 Mar 103 9:21:48-PST.

Query sequence being compared: US-08-828-922-1 (1-350)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-08-828-922-1 (1-350) with:
File: US09856836.pep

```

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
E 5-
O -
U -
N -
C -
E -
S 0-
SCORE 0 37 74 111 148 185 222 259 296 333
STDEV

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PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 168
Mismatch penalty 1
Gap penalty 5.00 Joining penalty 20
Gap size penalty 0.05 Window size 350
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 333 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 351
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Opt.	Score	Sig.	Frame
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1. US-09-856-836-2	Sequence 2, Application US	351	333	339	0.00	0
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1. US-08-828-922-1 (1-350)
US-09-856-836-2 Sequence 2, Application US/09856836

Initial Score = 333 Optimized Score = 339 Significance = 0.00
Residue Identity = 96% Matches = 337 Mismatches = 9
Gaps = 1 Conservative Substitutions = 4

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X      10      20      30      40      50      60      70
MEMQPTLTCSGHTRPVVDLAFSGITPYGFLLISACKDGPMLRGDGTGDMIGTFLGKGAWGATLNKDAT
|||||
MAMQPTLTCSGHTRPVVDLAFSGITPYGFLLISACKDGPMLRGDGTGDMIGTFLGKGAWGATLNKDAT
X      10      20      30      40      50      60      70

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      80      90     100     110     120     130     140
KAATAADFTAKYWDVAVSGDELMTLAKHIVKTVDFPTODSNYLLTGQDKLRLIYDLNKPFAEPKEISGHTS
|||||
KAATAADFTAKYWDVAVSGDELMTLAKHIVKTVDFPTODSNYLLTGQDKLRLIYDLNKPFAEPKEISGHTS
      80      90     100     110     120     130     140

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      150     160     170     180     190     200     210
GIRKALMCSDDKQIILSADDKTYVLMWDMHATMTVEKSLNFMNVSMSMEYIEGELLVYTGRSIAFSAVSLDP
|||||
GIRKALMCSDDKQIILSADDKTYVLMWDMHATMTVEKSLNFMNVSMSMEYIEGELLVYTGRSIAFSAVSLDP
      150     160     170     180     190     200     210

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      220     230     240     250     260     270     280
IKSFEAPATINSASLHPEKEFLVAGGEDFKLYKYDYNNGSEELBSYKGHGPHCVAFSPDGELVAGSGEDGT
|||||
IKSFEAPATINSASLHPEKEFLVAGGEDFKLYKYDYNNGSEELBSYKGHGPHCVAFSPDGELVAGSGEDGT
      220     230     240     250     260     270     280

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      290     300     310     320     330     340     350
LRLMOTVVGKTYGLMKCVLPBEDSGELAPKIGFPTTBEEL-ETIASNSDSCIPSPADVKA
|||||
LRLMOTVVGKTYGLMKCVLPBEDSGELAPKIGFPTTBEEL-ETIASNSDSCIPSPADVKA
      290     300     310     320     330     340     350

```